

AMENDMENTS TO THE SPECIFICATION

At page 16, paragraph 0034: An evolutionary distance matrix may be formed by converting each alignment score in the alignment score matrix to a distance. As one ordinarily skilled the art appreciates, the higher an alignment score is between two sequences, the more evolutionarily similar those two sequences are. In the limit of perfect alignment, two sequences may be said to have an evolutionary distance equal to zero between them. One method used by the methods according to the invention determines an evolutionary distance

between two sequences, i and j , according to $d_{i,j} = 1 - I_{i,j}$ where $I_{i,j} = \frac{S_{i,j}}{L}$.

$S_{i,j}$ is referred to as the fractional identity score. $S_{i,j}$ is the alignment score formed by summing the pairwise residue alignments along the highest scoring alignment that may be formed between i and j . L is the length of the alignment including gaps. In order to illustrate this method consider the following alignment between two exemplary sequences: NEQKRMPSRKFC (SEQ ID NO:1) and NEQKRRK (SEQ ID NO:2). Assume the optimal alignment between these two sequences is:

NEQKRMPSRKFC

NEQKR____RK__

Accordingly, $S_{i,j} = 7$, $L = 12$, $I_{i,j} = .583$ and $d_{i,j} = .417$.

If Applicants can do anything more to expedite this application, please contact the undersigned at (310) 788-3218.

Respectfully submitted,
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Date: February 28, 2006



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